

#11



P010

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/031,021

DATE: 08/08/2002  
TIME: 23:58:21

Input Set : N:\Crf3\08062002\J031021.raw  
Output Set: N:\CRF4\08082002\J031021.raw

1 <110> APPLICANT: GABANT, Philippe  
2 ROSCAM-SZPIRER, Josiane  
3 <120> TITLE OF INVENTION: NON-HUMAN GENETICALLY MODIFIED MAMMAL LACKING THE ALPHA-FETOPROTEIN  
4 <130> FILE REFERENCE: VANM243.1APC1  
5 <140> CURRENT APPLICATION NUMBER: US/10/031,021  
6 <141> CURRENT FILING DATE: 2002-01-14  
7 <150> PRIOR APPLICATION NUMBER: PCT/BE00/00081  
8 <151> PRIOR FILING DATE: 2000-07-11  
9 <160> NUMBER OF SEQ ID NOS: 8  
10 <170> SOFTWARE: PatentIn version 3.1  
12 <210> SEQ ID NO: 1  
13 <211> LENGTH: 31  
14 <212> TYPE: DNA  
15 <213> ORGANISM: Artificial Sequence  
16 <220> FEATURE:  
17 <223> OTHER INFORMATION: N-Mer1 primer  
18 <400> SEQUENCE: 1  
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21 <210> SEQ ID NO: 2  
22 <211> LENGTH: 29  
23 <212> TYPE: DNA  
24 <213> ORGANISM: Artificial Sequence  
25 <220> FEATURE:  
26 <223> OTHER INFORMATION: Description of Artificial Sequence: X-exon1 primer  
27 <400> SEQUENCE: 2  
28 agactcgagg gatgagggaa gcgggtgtg 29  
30 <210> SEQ ID NO: 3  
31 <211> LENGTH: 21  
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33 <213> ORGANISM: Artificial Sequence  
34 <220> FEATURE:  
35 <223> OTHER INFORMATION: Description of Artificial Sequence: afp#1 primer  
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39 <210> SEQ ID NO: 4  
40 <211> LENGTH: 20  
41 <212> TYPE: DNA  
42 <213> ORGANISM: Artificial Sequence  
43 <220> FEATURE:  
44 <223> OTHER INFORMATION: Description of Artificial Sequence: afp#2 primer  
45 <400> SEQUENCE: 4  
46 gaaaatagct cccaaagtac 20  
48 <210> SEQ ID NO: 5

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49 <211> LENGTH: 22  
50 <212> TYPE: DNA  
51 <213> ORGANISM: Artificial Sequence  
52 <220> FEATURE:  
53 <223> OTHER INFORMATION: Description of Artificial Sequence: lacZ#1 primer  
54 <400> SEQUENCE: 5  
55 acaacgtcgt gactggaaa ac 22  
57 <210> SEQ ID NO: 6  
58 <211> LENGTH: 18  
59 <212> TYPE: DNA  
60 <213> ORGANISM: Artificial Sequence  
61 <220> FEATURE:  
62 <223> OTHER INFORMATION: Description of Artificial Sequence: lacZ#2 primer  
63 <400> SEQUENCE: 6  
64 taatggata ggttacgt 18  
66 <210> SEQ ID NO: 7  
67 <211> LENGTH: 2009  
68 <212> TYPE: DNA  
69 <213> ORGANISM: Apodemus  
70 <220> FEATURE:  
71 <221> NAME/KEY: CDS  
72 <222> LOCATION: (42)..(1856)  
73 <223> OTHER INFORMATION:  
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75 tcccaacttcc agcaactgcct gcggtaaagg aacaaggcagc c atg aag tgg atc aca 56  
76 Met Lys Trp Ile Thr  
77 1 5  
78 ccc gct tcc ctc atc ctc ctg cta cat ttc gct gcg tcc aaa gca ttg 104  
79 Pro Ala Ser Leu Ile Leu Leu Leu His Phe Ala Ala Ser Lys Ala Leu  
80 10 15 20  
81 cac gaa aat gag ttt ggg ata gct tcc acg tta gat tcc tcc cag tgc 152  
82 His Glu Asn Glu Phe Gly Ile Ala Ser Thr Leu Asp Ser Ser Gln Cys  
83 25 30 35  
84 gtg acg gag aat gtg ctt agc ata gct acc atc acc ttt acc cag 200  
85 Val Thr Glu Lys Asn Val Leu Ser Ile Ala Thr Ile Thr Phe Thr Gln  
86 40 45 50  
87 ttt gtt ccg gaa gcc acc gag gag gaa gtg aac aaa atg act agc gat 248  
88 Phe Val Pro Glu Ala Thr Glu Glu Val Asn Lys Met Thr Ser Asp  
89 55 60 65  
90 gtg ttg gct gca atg aag aaa aac tct ggc gat ggg tgt tta gaa agc 296  
91 Val Leu Ala Ala Met Lys Lys Asn Ser Gly Asp Gly Cys Leu Glu Ser  
92 70 75 80 85  
93 cag cta tct gtg ttt ctg gat gaa att tgc cat gag acg gaa ctc tct 344  
94 Gln Leu Ser Val Phe Leu Asp Glu Ile Cys His Glu Thr Glu Leu Ser  
95 90 95 100  
96 aac aag tat gga ctc tca ggc tgc tgc agc caa agt gga gtg gaa aga 392  
97 Asn Lys Tyr Gly Leu Ser Gly Cys Cys Ser Gln Ser Gly Val Glu Arg  
98 105 110 115  
99 cat cag tgt ctg ctg gca cgc aag aag act gct ccg gcc tct gtc cca 440

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100	His Gln Cys Leu Leu Ala Arg Lys Lys Thr Ala Pro Ala Ser Val Pro	
101	120 125 130	
102	ccc ttc cag ttt cca gaa cct gcc gag agt tgc aaa gca cat gaa gaa	488
103	Pro Phe Gln Phe Pro Glu Pro Ala Glu Ser Cys Lys Ala His Glu Glu	
104	135 140 145	
105	aac agg gca gtg ttc atg aac agg ttc atc tat gaa gtg tca agg agg	536
106	Asn Arg Ala Val Phe Met Asn Arg Phe Ile Tyr Glu Val Ser Arg Arg	
107	150 155 160 165	
108	aac ccc ttc atg tat gcc cca gcc att ctg tcc ttg gct gct cag tac	584
109	Asn Pro Phe Met Tyr Ala Pro Ala Ile Leu Ser Leu Ala Ala Gln Tyr	
110	170 175 180	
111	gac aag gtc gtt ctg gca tgc tgc aaa gct gac aac aag gag gag tgc	632
112	Asp Lys Val Val Leu Ala Cys Cys Lys Ala Asp Asn Lys Glu Glu Cys	
113	185 190 195	
114	ttc cag aca aag aga gca tcc att gca aag gaa tta aga gaa gga agc	680
115	Phe Gln Thr Lys Arg Ala Ser Ile Ala Lys Glu Leu Arg Glu Gly Ser	
116	200 205 210	
117	atg tta aat gag cat gta tgt tca gtg ata aga aaa ttt gga tcc cga	728
118	Met Leu Asn Glu His Val Cys Ser Val Ile Arg Lys Phe Gly Ser Arg	
119	215 220 225	
120	aac ctc cag gca aca acc att att aag cta agt caa aag tta act gaa	776
121	Asn Leu Gln Ala Thr Thr Ile Ile Lys Leu Ser Gln Lys Leu Thr Glu	
122	230 235 240 245	
123	gca aat ttt act gag att cag aag ctg gcc ctg gat gtg gct cac atc	824
124	Ala Asn Phe Thr Glu Ile Gln Lys Leu Ala Leu Asp Val Ala His Ile	
125	250 255 260	
126	cac gag gag tgt tgc caa gga aac tcg ctg gag tgt ctg cag gat ggg	872
127	His Glu Glu Cys Cys Gln Gly Asn Ser Leu Glu Cys Leu Gln Asp Gly	
128	265 270 275	
129	gaa aaa gtc atg aca tat ata tgt tct caa caa aat att ctg tca agc	920
130	Glu Lys Val Met Thr Tyr Ile Cys Ser Gln Gln Asn Ile Leu Ser Ser	
131	280 285 290	
132	aaa ata gca gag tgc tgc aaa tta ccc atg atc caa cta ggc ttc tgc	968
133	Lys Ile Ala Glu Cys Cys Lys Leu Pro Met Ile Gln Leu Gly Phe Cys	
134	295 300 305	
135	ata att cac gca gag aat ggc gtc aaa cct gaa ggc tta tct cta aat	1016
136	Ile Ile His Ala Glu Asn Gly Val Lys Pro Glu Gly Leu Ser Leu Asn	
137	310 315 320 325	
138	cca agc cag ttt ttg gga gac aga aat ttt gcc caa ttt tct tca gag	1064
139	Pro Ser Gln Phe Leu Gly Asp Arg Asn Phe Ala Gln Phe Ser Ser Glu	
140	330 335 340	
141	gaa aaa atc atg ttc atg gca agc ttt ctt cat gaa tac tca aga act	1112
142	Glu Lys Ile Met Phe Met Ala Ser Phe Leu His Glu Tyr Ser Arg Thr	
143	345 350 355	
144	cac ccc aac ctt cct gtc tca gtc att cta aga att gct aaa acg tac	1160
145	His Pro Asn Leu Pro Val Ser Val Ile Leu Arg Ile Ala Lys Thr Tyr	
146	360 365 370	
147	cag gaa ata ttg gag aag tgt tcc cag tct gga aat cta cct gga tgt	1208
148	Gln Glu Ile Leu Glu Lys Cys Ser Gln Ser Gly Asn Leu Pro Gly Cys	

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149	375	380	385	
150	cag gac aat ctg gaa gaa ttg cat aaa cac atc gag gag agc cag			1256
151	Gln Asp Asn Leu Glu Glu Leu His Lys His Ile Glu Glu Ser Gln			
152	390	395	400	405
153	gca ctg tcc aag caa agc tgc gct ctc tac cag acc tta gga gac tac			1304
154	Ala Leu Ser Lys Gln Ser Cys Ala Leu Tyr Gln Thr Leu Gly Asp Tyr			
155	410	415	420	
156	aaa tta caa aat ctg ttc ctt att ggt tac acg agg aaa gcc cct cag			1352
157	Lys Leu Gln Asn Leu Phe Leu Ile Gly Tyr Thr Arg Lys Ala Pro Gln			
158	425	430	435	
159	ctg acc tca gca gag ctg atc gac ctc acc ggg aag atg gtg agc att			1400
160	Leu Thr Ser Ala Glu Leu Ile Asp Leu Thr Gly Lys Met Val Ser Ile			
161	440	445	450	
162	gcc tcc acg tgc tgc cag ctc agc gag gag aaa tgg tcc ggc tgt ggt			1448
163	Ala Ser Thr Cys Cys Gln Leu Ser Glu Glu Lys Trp Ser Gly Cys Gly			
164	455	460	465	
165	gag gga atg gcc gac att ttc att gga cat ttg tgt ata agg aat gaa			1496
166	Glu Gly Met Ala Asp Ile Phe Ile Gly His Leu Cys Ile Arg Asn Glu			
167	470	475	480	485
168	gca agc cct gtg aac tct ggt atc agc cac tgc tgc aac tct tcg tat			1544
169	Ala Ser Pro Val Asn Ser Gly Ile Ser His Cys Cys Asn Ser Ser Tyr			
170	490	495	500	
171	tcc aac agg agg cta tgc atc acc agt ttt ctg agg gat gaa acc tat			1592
172	Ser Asn Arg Arg Leu Cys Ile Thr Ser Phe Leu Arg Asp Glu Thr Tyr			
173	505	510	515	
174	gcc cct ccc cca ttc tct gag gat aaa ttc atc ttc cac aag gat ctg			1640
175	Ala Pro Pro Phe Ser Glu Asp Lys Phe Ile Phe His Lys Asp Leu			
176	520	525	530	
177	tgc caa gct cag ggc aaa gcc cta cag acc atg aaa caa gag ctt ctc			1688
178	Cys Gln Ala Gln Gly Lys Ala Leu Gln Thr Met Lys Gln Glu Leu Leu			
179	535	540	545	
180	att aac ctg gtg aag caa aag cct gaa ctg aca gag gag cag ctg gcg			1736
181	Ile Asn Leu Val Lys Gln Lys Pro Glu Leu Thr Glu Glu Gln Leu Ala			
182	550	555	560	565
183	gct gtc act gca gat ttc tgc ggc ctt ttg gag aag tgc tgc aaa gcc			1784
184	Ala Val Thr Ala Asp Phe Ser Gly Leu Leu Glu Lys Cys Cys Lys Ala			
185	570	575	580	
186	cag gac cag gaa gtc tgt ttc aca gaa gag ggt cca aag ttg att tcc			1832
187	Gln Asp Gln Glu Val Cys Phe Thr Glu Glu Gly Pro Lys Leu Ile Ser			
188	585	590	595	
189	aaa act cgt gat gct ttg ggc gtt taaacatctc cagaaggaag agtggacaaa			1886
190	Lys Thr Arg Asp Ala Leu Gly Val			
191	600	605		
192	aaaatgtgtt gacgctttgg tgtgagcctt ttggcttaac tgtaactgct agtactttaa			1946
193	ccacatggtg aagatgtcca tgtgagattt ctatacctta gaaataaaaa ctttcaact			2006
194	att			2009
196	<210> SEQ ID NO: 8			
197	<211> LENGTH: 605			
198	<212> TYPE: PRT			

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199 <213> ORGANISM: Apodemus  
 200 <400> SEQUENCE: 8  
 201 Met Lys Trp Ile Thr Pro Ala Ser Leu Ile Leu Leu Leu His Phe Ala  
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 203 Ala Ser Lys Ala Leu His Glu Asn Glu Phe Gly Ile Ala Ser Thr Leu  
 204 20 25 30  
 205 Asp Ser Ser Gln Cys Val Thr Glu Lys Asn Val Leu Ser Ile Ala Thr  
 206 35 40 45  
 207 Ile Thr Phe Thr Gln Phe Val Pro Glu Ala Thr Glu Glu Glu Val Asn  
 208 50 55 60  
 209 Lys Met Thr Ser Asp Val Leu Ala Ala Met Lys Lys Asn Ser Gly Asp  
 210 65 70 75 80  
 211 Gly Cys Leu Glu Ser Gln Leu Ser Val Phe Leu Asp Glu Ile Cys His  
 212 85 90 95  
 213 Glu Thr Glu Leu Ser Asn Lys Tyr Gly Leu Ser Gly Cys Cys Ser Gln  
 214 100 105 110  
 215 Ser Gly Val Glu Arg His Gln Cys Leu Leu Ala Arg Lys Lys Thr Ala  
 216 115 120 125  
 217 Pro Ala Ser Val Pro Pro Phe Gln Phe Pro Glu Pro Ala Glu Ser Cys  
 218 130 135 140  
 219 Lys Ala His Glu Glu Asn Arg Ala Val Phe Met Asn Arg Phe Ile Tyr  
 220 145 150 155 160  
 221 Glu Val Ser Arg Arg Asn Pro Phe Met Tyr Ala Pro Ala Ile Leu Ser  
 222 165 170 175  
 223 Leu Ala Ala Gln Tyr Asp Lys Val Val Leu Ala Cys Cys Lys Ala Asp  
 224 180 185 190  
 225 Asn Lys Glu Glu Cys Phe Gln Thr Lys Arg Ala Ser Ile Ala Lys Glu  
 226 195 200 205  
 227 Leu Arg Glu Gly Ser Met Leu Asn Glu His Val Cys Ser Val Ile Arg  
 228 210 215 220  
 229 Lys Phe Gly Ser Arg Asn Leu Gln Ala Thr Thr Ile Ile Lys Leu Ser  
 230 225 230 235 240  
 231 Gln Lys Leu Thr Glu Ala Asn Phe Thr Glu Ile Gln Lys Leu Ala Leu  
 232 245 250 255  
 233 Asp Val Ala His Ile His Glu Glu Cys Cys Gln Gly Asn Ser Leu Glu  
 234 260 265 270  
 235 Cys Leu Gln Asp Gly Glu Lys Val Met Thr Tyr Ile Cys Ser Gln Gln  
 236 275 280 285  
 237 Asn Ile Leu Ser Ser Lys Ile Ala Glu Cys Cys Lys Leu Pro Met Ile  
 238 290 295 300  
 239 Gln Leu Gly Phe Cys Ile Ile His Ala Glu Asn Gly Val Lys Pro Glu  
 240 305 310 315 320  
 241 Gly Leu Ser Leu Asn Pro Ser Gln Phe Leu Gly Asp Arg Asn Phe Ala  
 242 325 330 335  
 243 Gln Phe Ser Ser Glu Glu Lys Ile Met Phe Met Ala Ser Phe Leu His  
 244 340 345 350  
 245 Glu Tyr Ser Arg Thr His Pro Asn Leu Pro Val Ser Val Ile Leu Arg  
 246 355 360 365  
 247 Ile Ala Lys Thr Tyr Gln Glu Ile Leu Glu Lys Cys Ser Gln Ser Gly

**VERIFICATION SUMMARY****PATENT APPLICATION: US/10/031,021****DATE: 08/08/2002****TIME: 23:58:22****Input Set : N:\Crf3\08062002\J031021.raw****Output Set: N:\CRF4\08082002\J031021.raw**